

FIG. 1

BLASTP - query = 147_TR1; Hit = swiss|O15393|TMS2_HUMAN

This hit is scoring at : 3e-66 (expectation value)

Alignment length (overlap) : 370

Identities : 38 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb

Q: 36 CDGVVDCKLKSDDELGCVRFWDKSLKLIYSGSSHQWLPICSSNWNDYSEKTCQQLGFES
 CDGV .C. .DE CVR. . . :L::YS.....W P:C...WN::Y....C::G:::
 H: 133 CDGVSHCPGGEDENRCVRLYGPNFILQMYSSQRKSWHPVCQDDWNENYGRAACRDMGYKN

AHRTTEVAHRDFANSFSILRYNST IQESLHRSE CPSQRYISLQCSHCGLRA
 . : : . D : .S S : : .N : : I : .L : .S : C : S : : .SL : C CG : . : :
 NFYSSQGIVDD SGSTSFMKLNTSAGNVDIYKKLYHSDACSSKAVVSLRCLACGVNLNSS

MTGRIVGGALASDSKWPWQVSLHFGTTHCGGTLIDAQWVLTAAHCFVVTREKVLEG---
 ...RIVGG. A ...WPWQVSLH. ...H:CGG::I...W::TAAHC. EK L..
 RQSRIVGGESALPGAWPWQVSLHVQNVHVCGGSIITPEWVTAAHCV EKPLNNPWH

TRYPSIN HIS

WKVYAGTSNLHQLPAAAS--IAEIIINSNYTDEEDDYDIALMRLSKETLSGEGICTP
 W...AG. . . : .A. : : : I : .NY : : : : DIALM:L.KPLT... : :C.P
 WTAFAFILRQSFMYGAGYQVQKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLP

RSPAPQPOHPLOPSHLSASVNSYPGPKASADKTSPLREVQVNLIDFKKENDYLVDYSYL
 . P LQP..L . : : : G : : : : KTS..L...V LI : : :CN. .VYD : : :
 N PGMMLOPEQL-CWISGWGATEEKGKTSEVLNAAKVLLIETQRCNSRYVDNLI

TPRMMCAGDLRGGRDSCQGDSCGGLVCEQNNRWYLAGVTSWGTGCGQRNKPVGYYTKVTEV
 TP.M:CAG L:G. DSCQGDSCGGLV...NN W:L:G TSWG:GC... :PGVY .V. .
 TPAMICAGFLQGNVDSCQGDSCGGLVTSNNNIWWLIGDTSWGSACAKAYRPGVYGNVMVF

TRYPSIN SER

LPWIYSKMEA 389

.WIY.:M:A

TDWIYRQMK 490

FIG. 2

Prosite search results

PS00134	187->193 TRYPSIN_HIS	PDOC00124
PS00135	334->346 TRYPSIN_SER	PDOC00124

FIG. 3

BLOCKS search results

AC#	Description	Strength	Score
BL00495N AA#	Apple domain proteins. 325 AGdlrGGrDsCqGDSGGPLVCeqNnRWyLaGvTSW (SEQ ID NO:15)	1945	1582
BL01253G AA#	Type I fibronectin domain proteins. 332 rDsCQGDSGGPLVC (SEQ ID NO:16)	1641	1548
BL00134A AA#	Serine proteases, trypsin family, histidine p 175 CGGTLIDAQWVLTAHC (SEQ ID NO:17)	1500	1524
BL00021D AA#	Kringle domain proteins. 341 GPLVCEQNNRWYLaGVTSWGtGCGQRNKPGVYTKVTevLPWI (SEQ ID NO:18)	1556	1510
BL01253H AA#	Type I fibronectin domain proteins. 351 wYLaGvtSWGtGCGQRNKPGVYTKVTevLpWIysk (SEQ ID NO:19)	1765	1508
BL00021B AA#	Kringle domain proteins. 175 CGGTLIDaQWVLTAHCF (SEQ ID NO:20)	1547	1507
BL00495O AA#	Apple domain proteins. 360 GtGCGQRnkPGVYTKVTevlpWIysKmeA (SEQ ID NO:21)	1756	1383
BL00134B AA#	Serine proteases, trypsin family, histidine p 333 DSCQGDSGGPLVCEqNNRWYLAGV (SEQ ID NO:22)	1289	1299
BL01209 AA#	LDL-receptor class A (LDLRA) domain proteins. 35 CDGVVDCKlKSDE (SEQ ID NO:23)	1413	1274
BL01253F AA#	Type I fibronectin domain proteins. 288 AdktSpFLREvQVnLidfkKCndylVYdSylTPrMmCAG (SEQ ID NO:24)	1693	1270
BL00495L AA#	Apple domain proteins. 209 tSnlhqlpeaaSlaEIIInsNYtdeEddyDIALmrLskP (SEQ ID NO:25)	1947	1263
BL00134C AA#	Serine proteases, trypsin family, histidine p 369 PGVYTKVTEVLPWI (SEQ ID NO:26)	1245	1254
BL01253D AA#	Type I fibronectin domain proteins. 175 CGGtLIdaqWVLTA (SEQ ID NO:27)	1398	1217

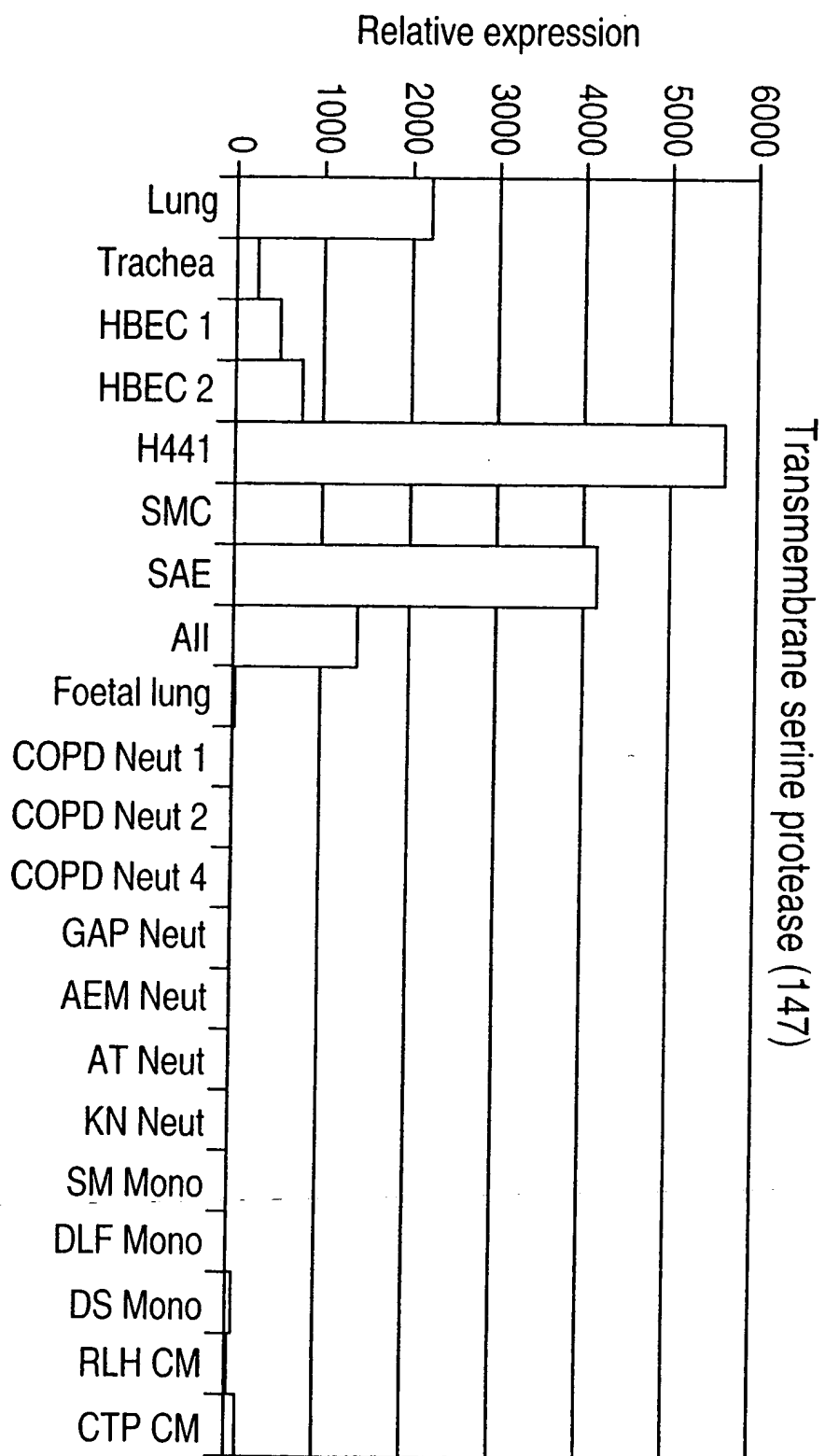


FIG. 4

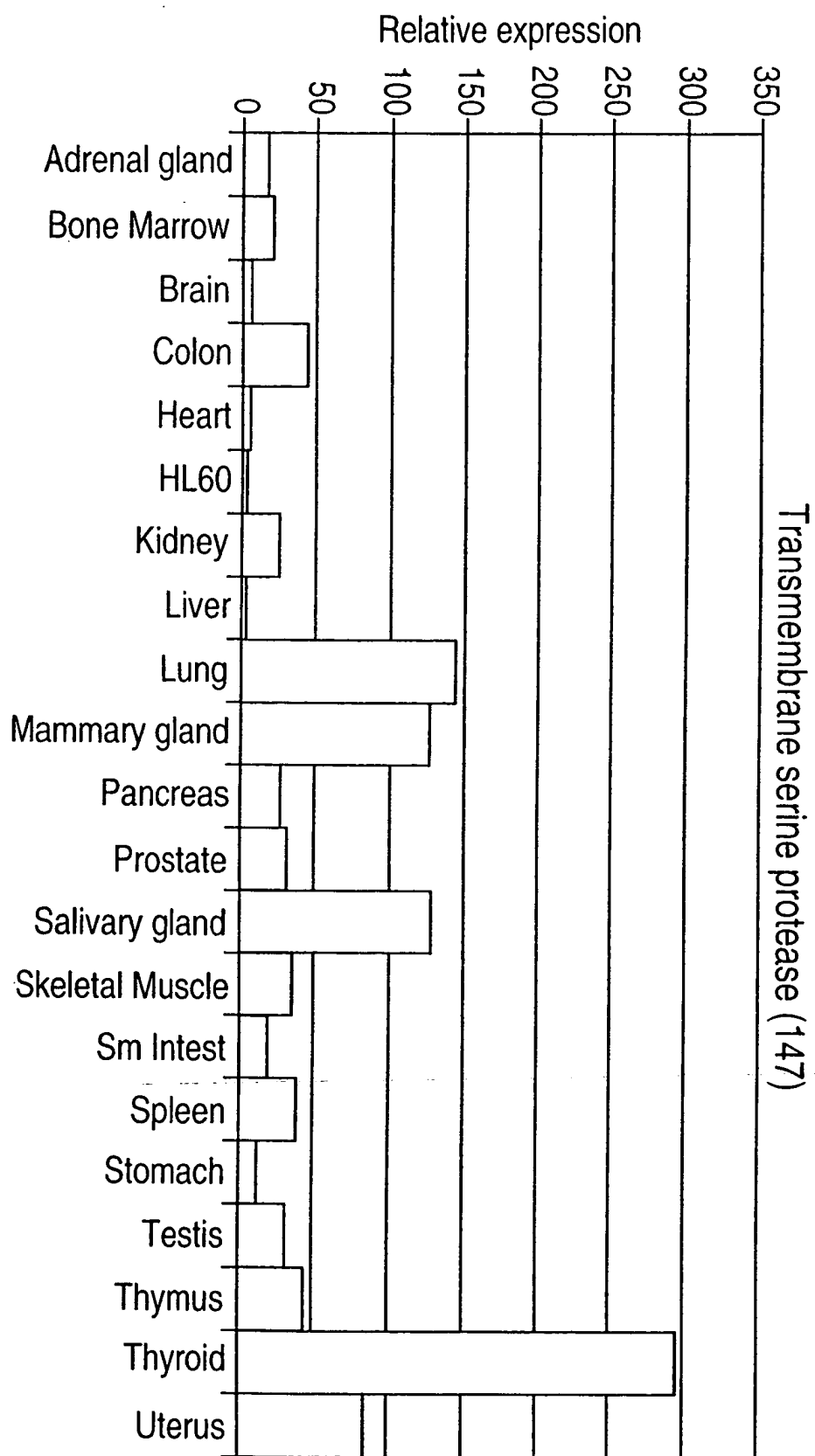
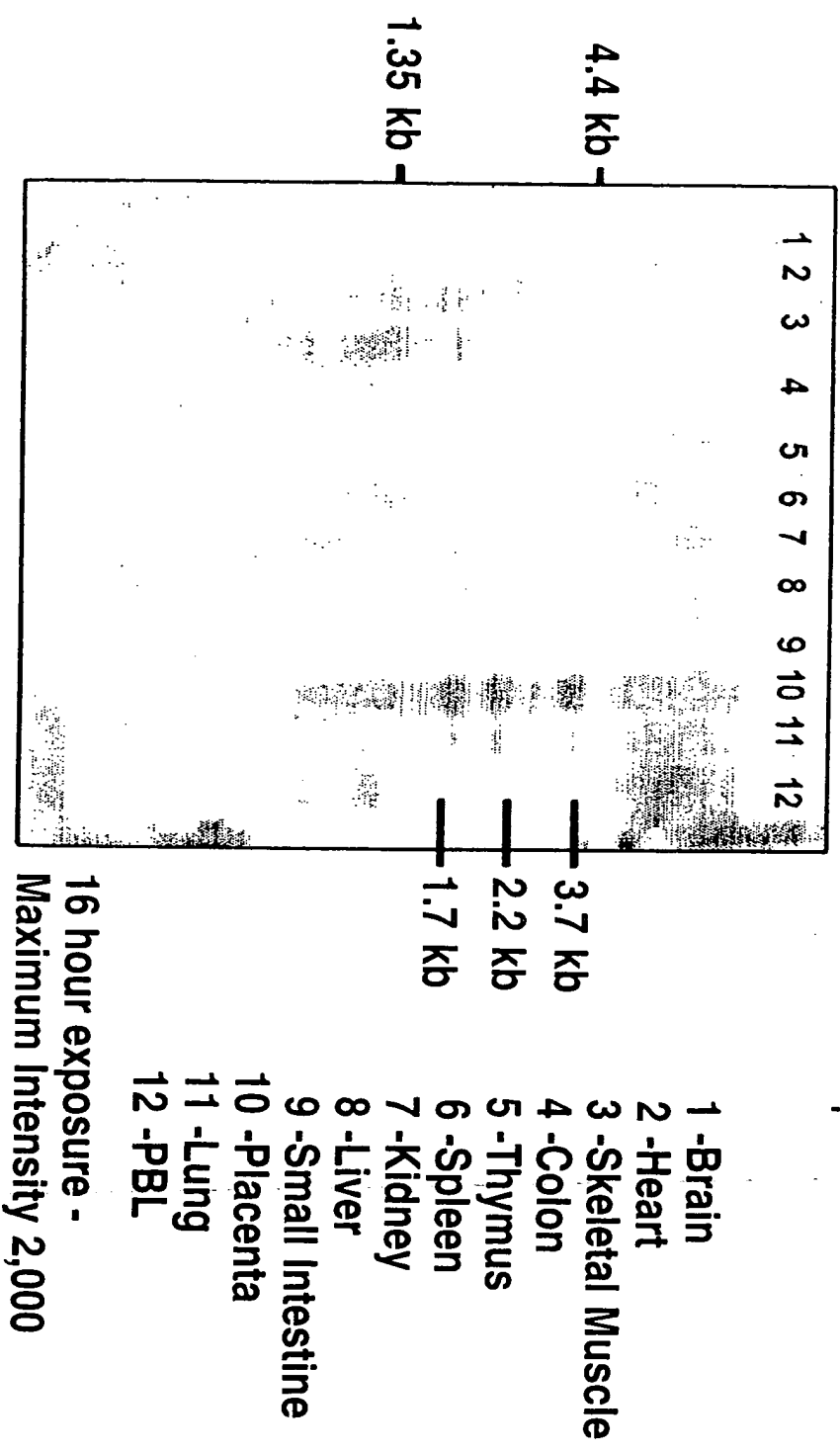


FIG. 5

FIG. 6

LBRI -147 - Transmembrane serine protease



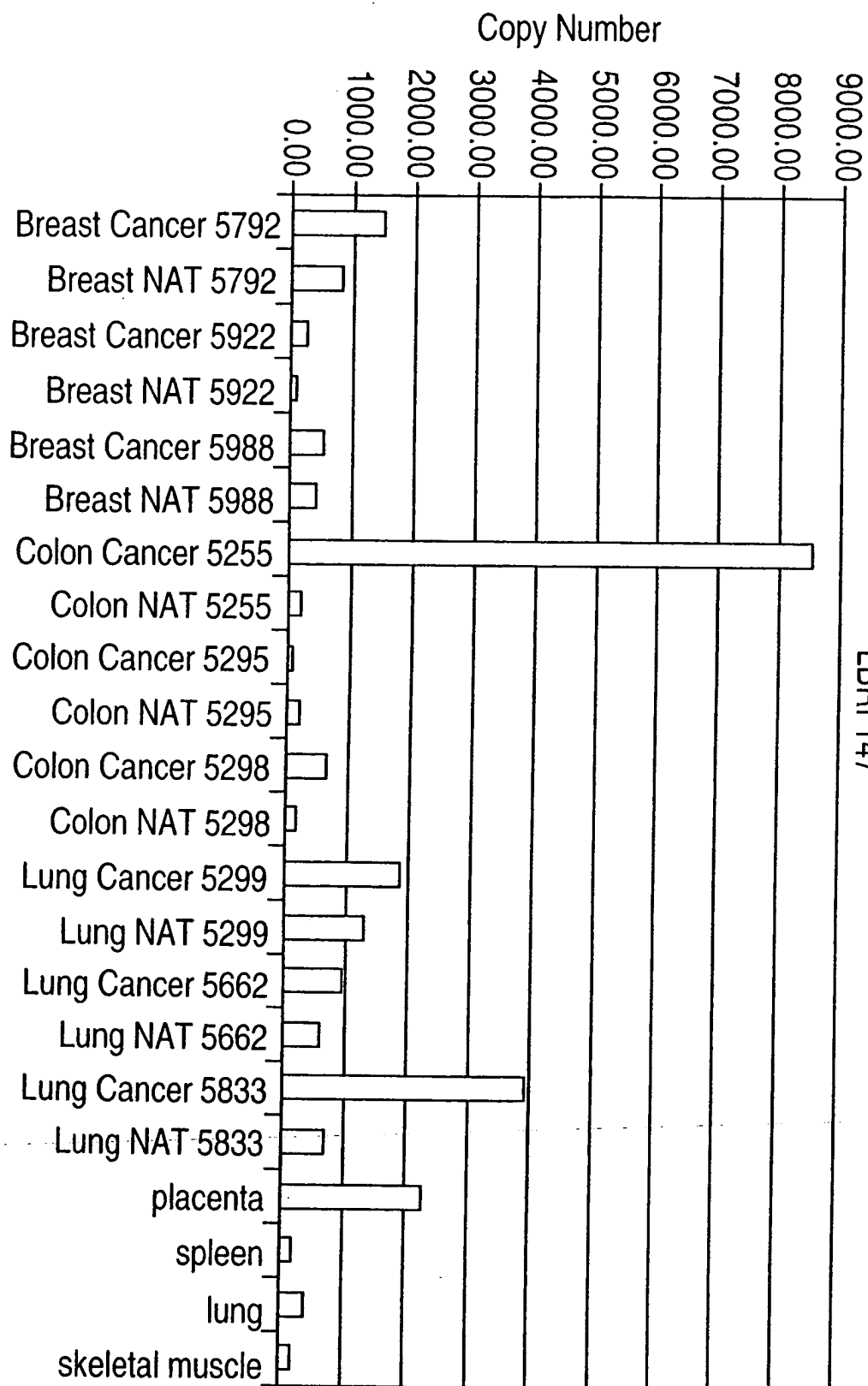


FIG. 7
LBRI 147

FIG. 8
LBRI 147: Fold Change

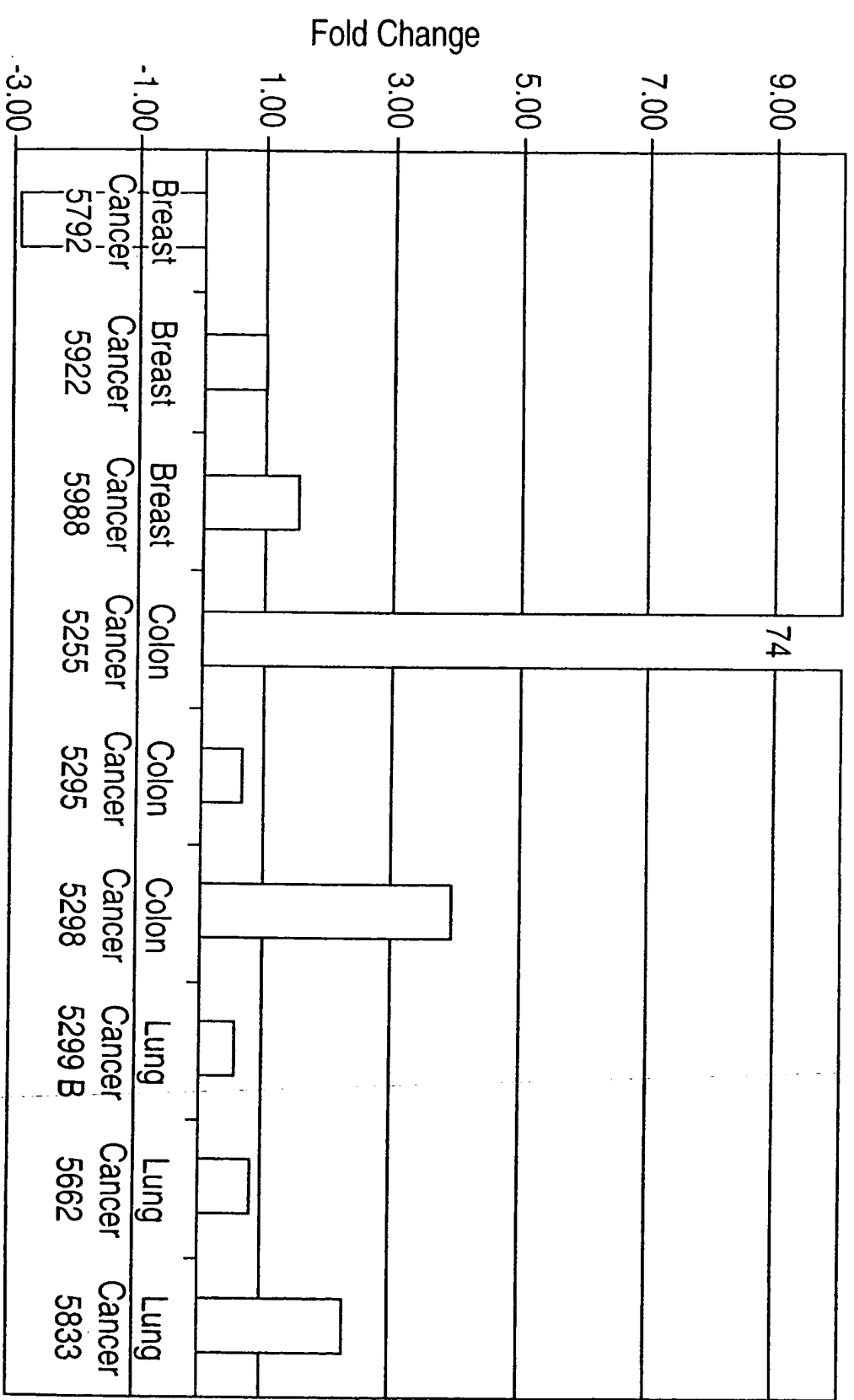


FIG. 9

